Class 11: Structural Bioinformatics pt2

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AlphaFold DB

The EBI maintains the largest database of AlphaFold structure prediction models at: https://alphafold.ebi.ac.uk

From last class (before Halloween) we saw that the PDB had 244,290 (Oct 2025)

The total number of protein sequences in UniProtKB is 199,579,901

> **Key Point**: This is a tiny fraction of sequence space that has structural coverage (0.12%)

```
244290/199579901 * 100
```

```
[1] 0.1224021
```

AFDB is attempting to address this gap…

There are two “Quality Scpres” from AlphaFold: one for residues (i.e. each amino acid) called **pLDDT** score, the other **PAE** score measures the confidence in the relative position of the residues (i.e.every pair of residues).

Generating your own structure predictions

Image of all 5 models

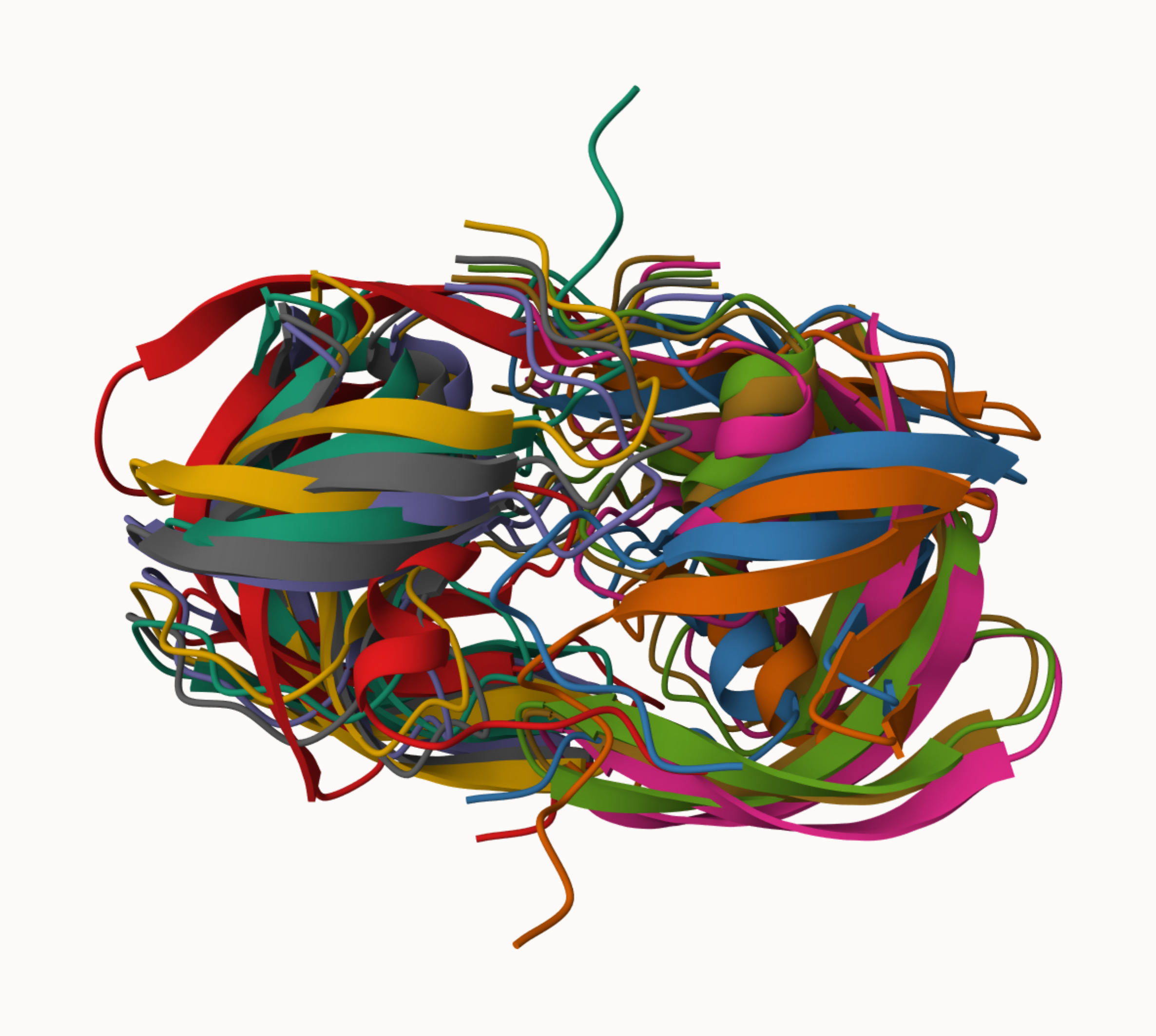
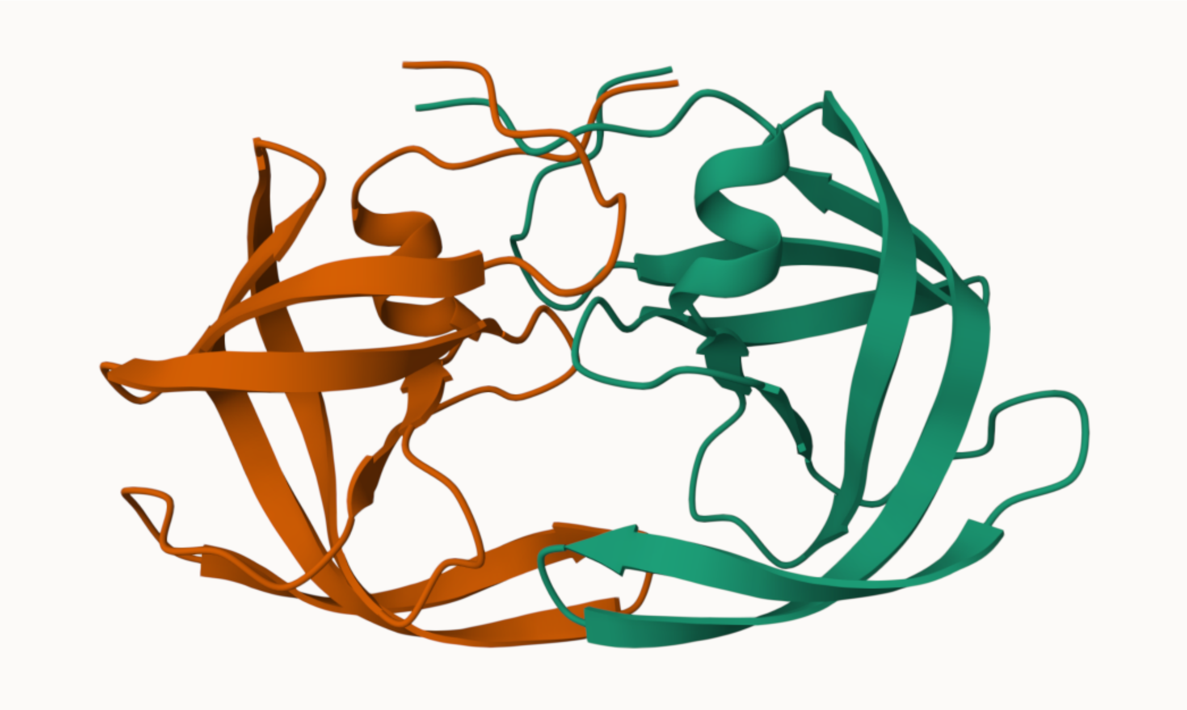
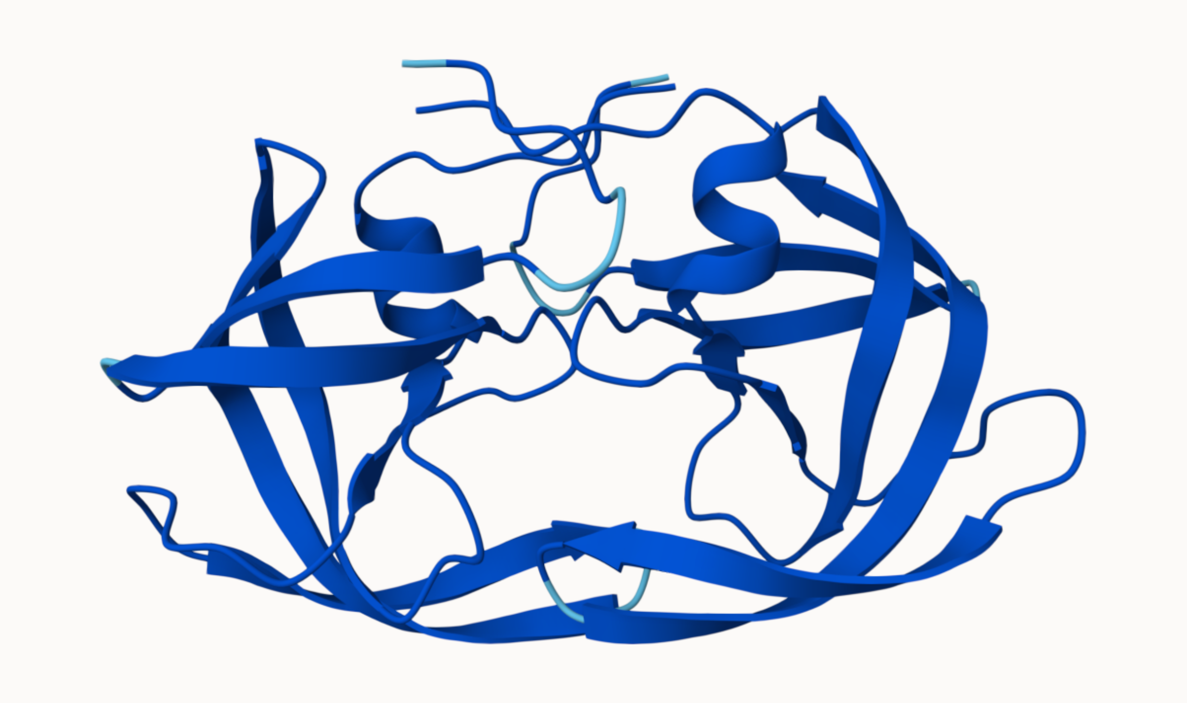


Image of 1st models



pLDDT score of 1st model



pLDDT score of 5th model

Custom analysis of resulting models in R

Read key result files into R. The first thing I need to know is what my results directory/folder is called (i.e. it name is different for every AlphaFold run/job)

```r
results_dir <- "HIVPR_Dimer_23119/"

# File names for all PDB models
pdb_files <- list.files(path=results_dir,
                        pattern="*.pdb",
                        full.names = TRUE)

# Print our PDB file names
basename(pdb_files)
```

```
[1] "HIVPR_Dimer_23119_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb"
[2] "HIVPR_Dimer_23119_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb"
[3] "HIVPR_Dimer_23119_unrelaxed_rank_003_alphafold2_multimer_v3_model_1_seed_000.pdb"
[4] "HIVPR_Dimer_23119_unrelaxed_rank_004_alphafold2_multimer_v3_model_5_seed_000.pdb"
[5] "HIVPR_Dimer_23119_unrelaxed_rank_005_alphafold2_multimer_v3_model_3_seed_000.pdb"
```

```r
library(bio3d)

m1 <- read.pdb(pdb_files[1])
m1
```

```

 Call:  read.pdb(file = pdb_files[1])

   Total Models#: 1
     Total Atoms#: 1514,  XYZs#: 4542  Chains#: 2  (values: A B)

     Protein Atoms#: 1514  (residues/Calpha atoms#: 198)
     Nucleic acid Atoms#: 0  (residues/phosphate atoms#: 0)

     Non-protein/nucleic Atoms#: 0  (residues: 0)
     Non-protein/nucleic resid values: [ none ]

   Protein sequence:
      PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYD
      QILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPQITLWQRPLVTIKIGGQLKE
      ALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTP
      VNIIGRNLLTQIGCTLNF

+ attr: atom, xyz, calpha, call
```

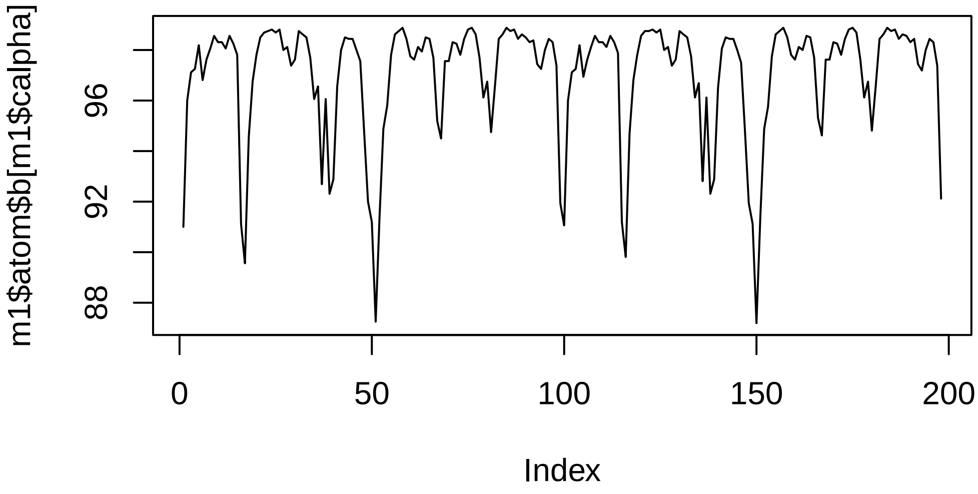
```r
head(m1$atom)
```

```
  type eleno elety  alt resid chain resno insert       x     y     z o  b segid
1 ATOM     1     N <NA>   PRO     A     1   <NA> -17.516 3.072 5.164 1 91  <NA>
2 ATOM     2    CA <NA>   PRO     A     1   <NA> -17.750 2.633 3.787 1 91  <NA>
3 ATOM     3     C <NA>   PRO     A     1   <NA> -16.938 1.399 3.412 1 91  <NA>
4 ATOM     4    CB <NA>   PRO     A     1   <NA> -17.328 3.844 2.953 1 91  <NA>
5 ATOM     5     O <NA>   PRO     A     1   <NA> -15.969 1.066 4.098 1 91  <NA>
6 ATOM     6    CG <NA>   PRO     A     1   <NA> -17.188 4.957 3.941 1 91  <NA>
  elesy charge
1     N   <NA>
2     C   <NA>
3     C   <NA>
4     C   <NA>
5     O   <NA>
6     C   <NA>
```

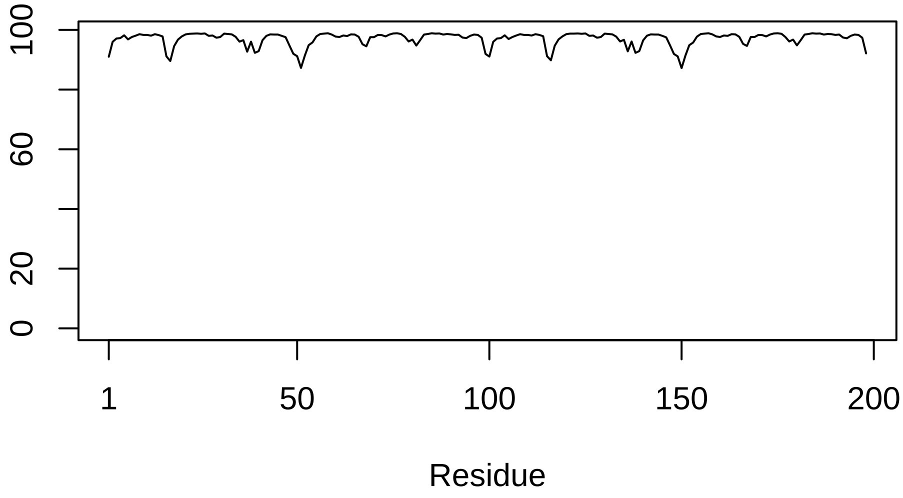
```r
m1$atom$b[m1$calpha]
```

```
  [1] 91.00 96.00 97.12 97.25 98.19 96.81 97.62 98.06 98.56 98.31 98.31 98.06
 [13] 98.56 98.25 97.81 91.12 89.56 94.56 96.75 97.81 98.50 98.69 98.75 98.81
 [25] 98.69 98.81 98.00 98.12 97.38 97.62 98.75 98.62 98.50 97.69 96.06 96.56
 [37] 92.69 96.06 92.31 92.88 96.56 98.00 98.50 98.44 98.44 98.00 97.56 94.75
 [49] 92.00 91.19 87.25 91.38 94.88 95.81 97.81 98.62 98.75 98.88 98.44 97.75
 [61] 97.62 98.12 97.94 98.50 98.44 97.69 95.19 94.50 97.56 97.56 98.31 98.25
 [73] 97.81 98.44 98.81 98.88 98.62 97.69 96.12 96.75 94.75 96.56 98.44 98.62
 [85] 98.88 98.75 98.81 98.44 98.62 98.50 98.31 98.38 97.44 97.25 98.00 98.44
 [97] 98.31 97.38 91.94 91.06 96.00 97.12 97.25 98.19 96.94 97.62 98.12 98.56
[109] 98.31 98.31 98.12 98.56 98.31 97.88 91.19 89.81 94.69 96.81 97.81 98.56
[121] 98.75 98.75 98.81 98.69 98.81 98.00 98.12 97.38 97.62 98.75 98.62 98.50
[133] 97.75 96.12 96.69 92.81 96.12 92.31 92.88 96.50 98.06 98.50 98.44 98.44
[145] 98.00 97.50 94.81 91.94 91.12 87.19 91.38 94.88 95.75 97.75 98.62 98.75
[157] 98.88 98.50 97.81 97.62 98.12 98.00 98.56 98.50 97.69 95.31 94.62 97.62
[169] 97.62 98.31 98.25 97.81 98.44 98.81 98.88 98.69 97.62 96.12 96.75 94.81
[181] 96.56 98.44 98.62 98.88 98.75 98.81 98.44 98.62 98.56 98.31 98.44 97.44
[193] 97.19 98.00 98.44 98.31 97.38 92.12
```

```r
plot(m1$atom$b[m1$calpha], typ = "l")
```



```
plot.bio3d(m1$atom$b[m1$calpha], typ = "l")
```



Residue conservation from alignment file

Find the large AlphaFold alignment file

```
aln_file <- list.files(path=results_dir,
                       pattern=".a3m$",
                        full.names = TRUE)
aln_file
```

```
[1] "HIVPR_Dimer_23119//HIVPR_Dimer_23119.a3m"
```

Read this into R

```
aln <- read.fasta(aln_file[1], to.upper = TRUE)
```

```
[1] " ** Duplicated sequence id's: 101 **"
[2] " ** Duplicated sequence id's: 101 **"
```

How many sequences are in this alignment

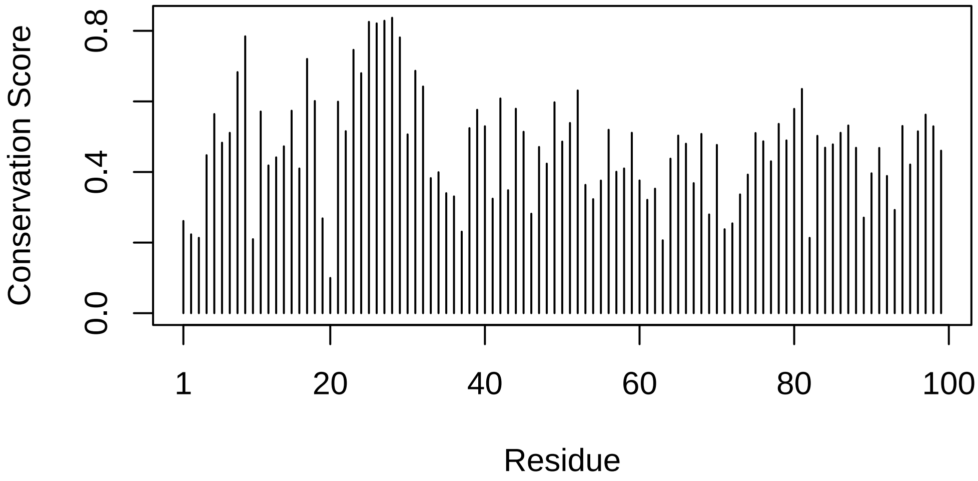
```
dim(aln$ali)
```

```
[1] 5397  132
```

We can score residue conservation in the alignment with the conserv() function.

```
sim <- conserv(aln)
```

```
plotb3(sim[1:99], ylab="Conservation Score")
```



```r
con <- consensus(aln, cutoff = 0.9)
con$seq
```

```
  [1] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [19] "-" "-" "-" "-" "-" "-" "D" "T" "G" "A" "-" "-" "-" "-" "-" "-" "-" "-"
 [37] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [55] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [73] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [91] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[109] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[127] "-" "-" "-" "-" "-" "-"
```